#4
8/21/00

RAW SEQUENCE LISTING   DATE: 08/21/2000
PATENT APPLICATION: US/09/540,245   TIME: 12:44:22

Input Set : A:\09540245.txt
Output Set: N:\CRF3\08212000\I540245.raw

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  5 <110> APPLICANT: Goodman, Corey
  7         Kid, Thomas
  9         Brose, Katja
 11         Tessier-Lavigne, Marc
 15 <120> TITLE OF INVENTION: Modulating Robo: Ligand Interactions
 19 <130> FILE REFERENCE: B98-031-3
 23 <140> CURRENT APPLICATION NUMBER: 09/540,245
 25 <141> CURRENT FILING DATE: 2000-03-31
 29 <150> PRIOR APPLICATION NUMBER: 09/191,647
 31 <151> PRIOR FILING DATE: 1998-11-13
 35 <150> PRIOR APPLICATION NUMBER: 60/081,057
 37 <151> PRIOR FILING DATE: 1998-04-07
 41 <160> NUMBER OF SEQ ID NOS: 14
 45 <170> SOFTWARE: PatentIn Ver. 2.0
 49 <210> SEQ ID NO: 1
 51 <211> LENGTH: 4758
 53 <212> TYPE: DNA
 55 <213> ORGANISM: human
 59 <220> FEATURE:
 61 <221> NAME/KEY: CDS
 63 <222> LOCATION: (1)..(4575)
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 71 Met Arg Gly Val Gly Trp Gln Met Leu Ser Leu Ser Leu Gly Leu Val
 73  1               5                  10                  15
 77 ctg gcg atc ctg aac aag gtg gca ccg cag gcg tgc ccg gcg cag tgc    96
 79 Leu Ala Ile Leu Asn Lys Val Ala Pro Gln Ala Cys Pro Ala Gln Cys
 81              20                  25                  30
 85 tct tgc tcg ggc agc aca gtg gac tgt cac ggg ctg gcg ctg cgc agc   144
 87 Ser Cys Ser Gly Ser Thr Val Asp Cys His Gly Leu Ala Leu Arg Ser
 89          35                  40                  45
 93 gtg ccc agg aat atc ccc cgc aac acc gag aga ctg gat tta aat gga   192
 95 Val Pro Arg Asn Ile Pro Arg Asn Thr Glu Arg Leu Asp Leu Asn Gly
 97      50                  55                  60
101 aat aac atc aca aga att acg aag aca gat ttt gct ggt ctt aga cat   240
103 Asn Asn Ile Thr Arg Ile Thr Lys Thr Asp Phe Ala Gly Leu Arg His
105  65                  70                  75                  80
109 cta aga gtt ctt cag ctt atg gag aat aag att agc acc att gaa aga   288
111 Leu Arg Val Leu Gln Leu Met Glu Asn Lys Ile Ser Thr Ile Glu Arg
113              85                  90                  95
117 gga gca ttc cag gat ctt aaa gaa cta gag aga ctg cgt tta aac aga  ·336
119 Gly Ala Phe Gln Asp Leu Lys Glu Leu Glu Arg Leu Arg Leu Asn Arg
121             100                 105                 110
125 aat cac ctt cag ctg ttt cct gag ttg ctg ttt ctt ggg act gcg aag   384
127 Asn His Leu Gln Leu Phe Pro Glu Leu Leu Phe Leu Gly Thr Ala Lys
129         115                 120                 125
133 cta tac agg ctt gat ctc agt gaa aac caa att cag gca atc cca agg   432
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135 Leu Tyr Arg Leu Asp Leu Ser Glu Asn Gln Ile Gln Ala Ile Pro Arg
137     130                 135                 140
141 aaa gct ttc cgt ggg gca gtt gac ata aaa aat ttg caa ctg gat tac    480
143 Lys Ala Phe Arg Gly Ala Val Asp Ile Lys Asn Leu Gln Leu Asp Tyr
145 145                 150                 155                 160
149 aac cag atc agc tgt att gaa gat ggg gca ttc agg gct ctc cgg gac    528
151 Asn Gln Ile Ser Cys Ile Glu Asp Gly Ala Phe Arg Ala Leu Arg Asp
153                 165                 170                 175
157 ctg gaa gtg ctc act ctc aac aat aac aac att act aga ctt tct gtg    576
159 Leu Glu Val Leu Thr Leu Asn Asn Asn Asn Ile Thr Arg Leu Ser Val
161             180                 185                 190
165 gca agt ttc aac cat atg cct aaa ctt agg act ttt cga ctg cat tca    624
167 Ala Ser Phe Asn His Met Pro Lys Leu Arg Thr Phe Arg Leu His Ser
169             195                 200                 205
173 aac aac ctg tat tgt gac tgc cac ctg gcc tgg ctc tcc gac tgg ctt    672
175 Asn Asn Leu Tyr Cys Asp Cys His Leu Ala Trp Leu Ser Asp Trp Leu
177     210                 215     -           220
181 cgc aaa agg cct cgg gtt ggt ctg tac act cag tgt atg ggc ccc tcc    720
183 Arg Lys Arg Pro Arg Val Gly Leu Tyr Thr Gln Cys Met Gly Pro Ser
185 225                 230                 235                 240
189 cac ctg aga ggc cat aat gta gcc gag gtt caa aaa cga gaa ttt gtc    768
191 His Leu Arg Gly His Asn Val Ala Glu Val Gln Lys Arg Glu Phe Val
193             245 \               250                 255
197 tgc agt gat gag gaa gaa ggt cac cag tca ttt atg gct cct tct tgt    816
199 Cys Ser Asp Glu Glu Glu Gly His Gln Ser Phe Met Ala Pro Ser Cys
201             260                 265                 270
205 agt gtt ttg cac tgc cct gcc gcc tgt acc tgt agc aac aat atc gta    864
207 Ser Val Leu His Cys Pro Ala Ala Cys Thr Cys Ser Asn Asn Ile Val
209             275                 280                 285
213 gac tgt cgt ggg aaa ggt ctc act gag atc ccc aca aat ctt cca gag    912
215 Asp Cys Arg Gly Lys Gly Leu Thr Glu Ile Pro Thr Asn Leu Pro Glu
217         290                 295                 300
221 acc atc aca gaa ata cgt ttg gaa cag aac aca atc aaa gtc atc cct    960
223 Thr Ile Thr Glu Ile Arg Leu Glu Gln Asn Thr Ile Lys Val Ile Pro
225 305                 310                 315                 320
229 cct gga gct ttc tca cca tat aaa aag ctt aga cga att gac ctg agc   1008
231 Pro Gly Ala Phe Ser Pro Tyr Lys Lys Leu Arg Arg Ile Asp Leu Ser
233             325                 330                 335
237 aat aat cag atc tct gaa ctt gca cca gat gct ttc caa gga cta cgc   1056
239 Asn Asn Gln Ile Ser Glu Leu Ala Pro Asp Ala Phe Gln Gly Leu Arg
241             340                 345                 350
245 tct ctg aat tca ctt gtc ctc tat gga aat aaa atc aca gaa ctc ccc   1104
247 Ser Leu Asn Ser Leu Val Leu Tyr Gly Asn Lys Ile Thr Glu Leu Pro
249             355                 360                 365
253 aaa agt tta ttt gaa gga ctg ttt tcc tta cag ctc cta tta ttg aat   1152
255 Lys Ser Leu Phe Glu Gly Leu Phe Ser Leu Gln Leu Leu Leu Leu Asn
257     370                 375                 380
261 gcc aac aag ata aac tgc ctt cgg gta gat gct ttt cag gat ctc cac   1200
263 Ala Asn Lys Ile Asn Cys Leu Arg Val Asp Ala Phe Gln Asp Leu His
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265 385                   390                   395                   400
269 aac ttg aac ctt ctc tcc cta tat gac aac aag ctt cag acc atc gcc     1248
271 Asn Leu Asn Leu Leu Ser Leu Tyr Asp Asn Lys Leu Gln Thr Ile Ala
273              .          405                   410                   415
277 aag ggg acc ttt tca cct ctt cgg gcc att caa act atg cat ttg gcc     1296
279 Lys Gly Thr Phe Ser Pro Leu Arg Ala Ile Gln Thr Met His Leu Ala
281              420                   425                   430
285 cag aac ccc ttt att tgt gac tgc cat ctc aag tgg cta gcg gat tat     1344
287 Gln Asn Pro Phe Ile Cys Asp Cys His Leu Lys Trp Leu Ala Asp Tyr
289         435                   440                   445
293 ctc cat acc aac ccg att gag acc agt ggt gcc cgt tgc acc agc ccc     1392
295 Leu His Thr Asn Pro Ile Glu Thr Ser Gly Ala Arg Cys Thr Ser Pro
297         450                   455                   460
301 cgc cgc ctg gca aac aaa aga att gga cag atc aaa agc aag aaa ttc     1440
303 Arg Arg Leu Ala Asn Lys Arg Ile Gly Gln Ile Lys Ser Lys Lys Phe
305 465                   470                   475                   480
309 cgt tgt tca ggt aca gaa gat tat cga tca aaa tta agt gga gac tgc     1488
311 Arg Cys Ser Gly Thr Glu Asp Tyr Arg Ser Lys Leu Ser Gly Asp Cys
313              485                   490                   495
317 ttt gcg gat ctg gct tgc cct gaa aag tgt cgc tgt gaa gga acc aca     1536
319 Phe Ala Asp Leu Ala Cys Pro Glu Lys Cys Arg Cys Glu Gly Thr Thr
321              500                   505                   510
325 gta gat tgc tct aat caa aag ctc aac aaa atc ccg gag cac att ccc     1584
327 Val Asp Cys Ser Asn Gln Lys Leu Asn Lys Ile Pro Glu His Ile Pro     .
329         515                   520                   525
333 cag tac act gca gag ttg cgt ctc aat aat aat gaa ttt acc gtg ttg     1632
335 Gln Tyr Thr Ala Glu Leu Arg Leu Asn Asn Asn Glu Phe Thr Val Leu
337         530                   535                   540
341 gaa gcc aca gga atc ttt aag aaa ctt cct caa tta cgt aaa ata aac     1680
343 Glu Ala Thr Gly Ile Phe Lys Lys Leu Pro Gln Leu Arg Lys Ile Asn
345 545                   550                   555                   560
349 ttt agc aac aat aag atc aca gat att gag gag gga gca ttt gaa gga     1728
351 Phe Ser Asn Asn Lys Ile Thr Asp Ile Glu Glu Gly Ala Phe Glu Gly
353              565                   570                   575
357 gca tct ggt gta aat gaa ata ctt ctt acg agt aat cgt ttg gaa aat     1776
359 Ala Ser Gly Val Asn Glu Ile Leu Leu Thr Ser Asn Arg Leu Glu Asn
361              580                   585                   590
365 gtg cag cat aag atg ttc aag gga ttg gaa agc ctc aaa act ttg atg     1824
367 Val Gln His Lys Met Phe Lys Gly Leu Glu Ser Leu Lys Thr Leu Met
369         595                   600                   605
373 ttg aga agc aat cga ata acc tgt gtg ggg aat gac agt ttc ata gga     1872
375 Leu Arg Ser Asn Arg Ile Thr Cys Val Gly Asn Asp Ser Phe Ile Gly
377         610                   615                   620
381 ctc agt tct gtg cgt ttg ctt tct ttg tat gat aat caa att act aca     1920
383 Leu Ser Ser Val Arg Leu Leu Ser Leu Tyr Asp Asn Gln Ile Thr Thr
385 625                   630                   635                   640
389 gtt gca cca ggg gca ttt gat act ctc cat tct tta tct act cta aac     1968
391 Val Ala Pro Gly Ala Phe Asp Thr Leu His Ser Leu Ser Thr Leu Asn
393         .          645                   650                   655
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397 ctc ttg gcc aat cct ttt aac tgt aac tgc tac ctg gct tgg ttg gga   2016
399 Leu Leu Ala Asn Pro Phe Asn Cys Asn Cys Tyr Leu Ala Trp Leu Gly
401         660             665             670
405 gag tgg ctg aga aag aag aga att gtc acg gga aat cct aga tgt caa   2064
407 Glu Trp Leu Arg Lys Lys Arg Ile Val Thr Gly Asn Pro Arg Cys Gln
409         675             680             685
413 aaa cca tac ttc ctg aaa gaa ata ccc atc cag gat gtg gcc att cag   2112
415 Lys Pro Tyr Phe Leu Lys Glu Ile Pro Ile Gln Asp Val Ala Ile Gln
417     690             695             700
421 gac ttc act tgt gat gac gga aat gat gac aat agt tgc tcc cca ctt   2160
423 Asp Phe Thr Cys Asp Asp Gly Asn Asp Asp Asn Ser Cys Ser Pro Leu
425 705             710             715             720
429 tct cgc tgt cct act gaa tgt act tgc ttg gat aca gtc gtc cga tgt   2208
431 Ser Arg Cys Pro Thr Glu Cys Thr Cys Leu Asp Thr Val Val Arg Cys
433             725             730             735
437 agc aac aag ggt ttg aag gtc ttg ccg aaa ggt att cca aga gat gtc   2256
439 Ser Asn Lys Gly Leu Lys Val Leu Pro Lys Gly Ile Pro Arg Asp Val
441             740             745             750
445 aca gag ttg tat ctg gat gga aac caa ttt aca ctg gtt ccc aag gaa   2304
447 Thr Glu Leu Tyr Leu Asp Gly Asn Gln Phe Thr Leu Val Pro Lys Glu
449         755             760             765
453 ctc tcc aac tac aaa cat tta aca ctt ata gac tta agt aac aac aga   2352
455 Leu Ser Asn Tyr Lys His Leu Thr Leu Ile Asp Leu Ser Asn Asn Arg
457     770             775             780
461 ata agc acg ctt tct aat cag agc ttc agc aac atg acc cag ctc ctc   2400
463 Ile Ser Thr Leu Ser Asn Gln Ser Phe Ser Asn Met Thr Gln Leu Leu
465 785             790             795             800
469 acc tta att ctt agt tac aac cgt ctg aga tgt att cct cct cgc acc   2448
471 Thr Leu Ile Leu Ser Tyr Asn Arg Leu Arg Cys Ile Pro Pro Arg Thr
473             805             810             815
477 ttt gat gga tta aag tct ctt cga tta ctt tct cta cat gga aat gac   2496
479 Phe Asp Gly Leu Lys Ser Leu Arg Leu Leu Ser Leu His Gly Asn Asp
481             820             825             830
485 att tct gtt gtg cct gaa ggt gct ttc aat gat ctt tct gca tta tca   2544
487 Ile Ser Val Val Pro Glu Gly Ala Phe Asn Asp Leu Ser Ala Leu Ser
489         835             840             845
493 cat cta gca att gga gcc aac cct ctt tac tgt gat tgt aac atg cag   2592
495 His Leu Ala Ile Gly Ala Asn Pro Leu Tyr Cys Asp Cys Asn Met Gln
497     850             855             860
501 tgg tta tcc gac tgg gtg aag tcg gaa tat aag gag cct gga att gct   2640
503 Trp Leu Ser Asp Trp Val Lys Ser Glu Tyr Lys Glu Pro Gly Ile Ala
505 865             870             875             880
509 cgt tgt gct ggt cct gga gaa atg gca gat aaa ctt tta ctc aca act   2688
511 Arg Cys Ala Gly Pro Gly Glu Met Ala Asp Lys Leu Leu Leu Thr Thr
513             885             890             895
517 ccc tcc aaa aaa ttt acc tgt caa ggt cct gtg gat gtc aat att cta   2736
519 Pro Ser Lys Lys Phe Thr Cys Gln Gly Pro Val Asp Val Asn Ile Leu
521             900             905             910
525 gct aag tgt aac ccc tgc cta tca aat ccg tgt aaa aat gat ggc aca   2784
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527 Ala Lys Cys Asn Pro Cys Leu Ser Asn Pro Cys Lys Asn Asp Gly Thr
529         915                 920                 925
533 tgt aat agt gat cca gtt gac ttt tac cga tgc acc tgt cca tat ggt   2832
535 Cys Asn Ser Asp Pro Val Asp Phe Tyr Arg Cys Thr Cys Pro Tyr Gly
537         930                 935                 940
541 ttc aag ggg cag gac tgt gat gtc cca att cat gcc tgc atc agt aac   2880
543 Phe Lys Gly Gln Asp Cys Asp Val Pro Ile His Ala Cys Ile Ser Asn
545 945                 950                 955                 960
549 cca tgt aaa cat gga gga act tgc cac tta aag gaa gga gaa gaa gat   2928
551 Pro Cys Lys His Gly Gly Thr Cys His Leu Lys Glu Gly Glu Glu Asp
553                 965                 970                 975
557 gga ttc tgg tgt att tgt gct gat gga ttt gaa gga gaa aat tgt gaa   2976
559 Gly Phe Trp Cys Ile Cys Ala Asp Gly Phe Glu Gly Glu Asn Cys Glu
561                 980                 985                 990
565 gtc aac gtt gat gat tgt gaa gat aat gac tgt gaa aat aat tct aca   3024
567 Val Asn Val Asp Asp Cys Glu Asp Asn Asp Cys Glu Asn Asn Ser Thr
569         995                 1000                1005
573 tgt gtc gat ggc att aat aac tac aca tgc ctt tgc cca cct gag tat   3072
575 Cys Val Asp Gly Ile Asn Asn Tyr Thr Cys Leu Cys Pro Pro Glu Tyr
577     1010                1015                1020
581 aca ggt gag ttg tgt gag gag aag ctg gac ttc tgt gcc cag gac ctg   3120
583 Thr Gly Glu Leu Cys Glu Glu Lys Leu Asp Phe Cys Ala Gln Asp Leu
585 1025                1030                1035                1040
589 aac ccc tgc cag cac gat tca aag tgc atc cta act cca aag gga ttc   3168
591 Asn Pro Cys Gln His Asp Ser Lys Cys Ile Leu Thr Pro Lys Gly Phe
593                 1045                1050                1055
597 aaa tgt gac tgc aca cca ggg tac gta ggt gaa cac tgc gac atc gat   3216
599 Lys Cys Asp Cys Thr Pro Gly Tyr Val Gly Glu His Cys Asp Ile Asp
601         1060                1065                1070
605 ttt gac gac tgc caa gac aac aag tgt aaa aac gga gcc cac tgc aca   3264
607 Phe Asp Asp Cys Gln Asp Asn Lys Cys Lys Asn Gly Ala His Cys Thr
609     1075                1080                1085
613 gat gca gtg aac ggc tat acg tgc ata tgc ccc gaa ggt tac agt ggc   3312
615 Asp Ala Val Asn Gly Tyr Thr Cys Ile Cys Pro Glu Gly Tyr Ser Gly
617     1090                1095                1100
621 ttg ttc tgt gag ttt tct cca ccc atg gtc ctc cct cgt acc agc ccc   3360
623 Leu Phe Cys Glu Phe Ser Pro Pro Met Val Leu Pro Arg Thr Ser Pro
625 1105                1110                1115                1120
629 tgt gat aat ttt gat tgt cag aat gga gct cag tgt atc gtc aga ata   3408
631 Cys Asp Asn Phe Asp Cys Gln Asn Gly Ala Gln Cys Ile Val Arg Ile
633                 1125                1130                1135
637 aat gag cca ata tgt cag tgt ttg cct ggc tat cag gga gaa aag tgt   3456
639 Asn Glu Pro Ile Cys Gln Cys Leu Pro Gly Tyr Gln Gly Glu Lys Cys
641                 1140                1145                1150
645 gaa aaa ttg gtt agt gtg aat ttt ata aac aaa gag tct tat ctt cag   3504
647 Glu Lys Leu Val Ser Val Asn Phe Ile Asn Lys Glu Ser Tyr Leu Gln
649         1155                1160                1165
653 att cct tca gcc aag gtt cgg cct cag acg aac ata aca ctt cag att   3552
655 Ile Pro Ser Ala Lys Val Arg Pro Gln Thr Asn Ile Thr Leu Gln Ile
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Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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L:1615 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5
L:1615 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:5
L:1627 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:5
L:1627 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:1627 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:1627 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5
M:340 Repeated in SeqNo=5
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L:2278 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8
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L:2278 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8
L:2278 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:8
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L:2320 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:2320 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8
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L:2332 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:8
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